

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 6915849
Number of Sequences: 113759
Number of extensions: 293459
Number of successful extensions: 1107
Number of sequences better than 10.0: 26
Number of HSP's better than 10.0 without gapping: 7
Number of HSP's successfully gapped in prelim test: 19
Number of HSP's that attempted gapping in prelim test: 1094
Number of HSP's gapped (non-prelim): 35
length of query: 121
length of database: 24,820,038
effective HSP length: 40
effective length of query: 81
effective length of database: 20269678
effective search space: 1641843918
effective search space used: 1641843918
T: 11
A: 40
X1: 15 (7.1 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 40 (21.8 bits)
S2: 59 (27.4 bits)
BLASTP 2.0.9 [May-07-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

Query= 78-8-3-E6-CL0_1C
(227 letters)

Database: /nfs/banks2/index/data/blast/smartSorted/PROT/homosapiens
113,759 sequences; 24,820,038 total letters

Searching.....done

Sequences producing significant alignments:			Score (bits)	E Value
GSP:Y35976	Y35976	Extended human secreted protein sequence, SEQ...	481	e-136
GSP:Y94263	Y94263	Human phospholipid binding protein 2, PLBP2.	476	e-134
GSP:Y11860	Y11860	Human 5' EST secreted protein SEQ ID No: 460.	258	6e-69
GSP:R27718	R27718	HCNP precursor protein #2. >GSP:R49943 R49943...	81	2e-15
GSP:R64268	R64268	Phosphatidylethanolamine binding protein.	81	2e-15
SP:P30086	PEBP_HUMAN	PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (...)	81	2e-15
GNP:S76773	S76773_1	neuropolypeptide h3 [human, brain, mRNA Par...	81	2e-15
GSP:Y11503	Y11503	Human 5' EST secreted protein SEQ ID No 325.	35	0.090
STR:AAF28940	AAF28940	HSPC262 (Fragment). >GNP:AF161380 AF16138...	35	0.090
STR:Q92508	Q92508	MYELOBLAST KIAA0233. >GNP:D87071 D87071_1 Hum...	30	3.0

>GSP:Y35976|Y35976|Extended human secreted protein sequence, SEQ ID
NO. 225. >GSP:Y64647|Y64647|Human
phosphatidylethanolamine-binding protein.
Length = 227

Score = 481 bits (1224), Expect = e-136
Identities = 227/227 (100%), Positives = 227/227 (100%)

Query: 1 MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV 60
MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV
Sbjct: 1 MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV 60

Query: 61 VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG 120
VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG
Sbjct: 61 VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG 120

Query: 121 ADLKKGKIQQQELSAQAPSPPAHSGFHRYPFFVYLQEGKVISLLPKENKTRGSWKMDRF 180
ADLKKGKIQQQELSAQAPSPPAHSGFHRYPFFVYLQEGKVISLLPKENKTRGSWKMDRF
Sbjct: 121 ADLKKGKIQQQELSAQAPSPPAHSGFHRYPFFVYLQEGKVISLLPKENKTRGSWKMDRF 180

Query: 181 LNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNQAEIAAC 227

LNRFLHGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNAEIAAC
 Sbjct: 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNAEIAAC 227

>GSP:Y94263|Y94263|Human phospholipid binding protein 2, PLBP2.
 Length = 227

Score = 476 bits (1213), Expect = e-134
 Identities = 225/227 (99%), Positives = 226/227 (99%)

Query: 1 MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV 60
 MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV
 Sbjct: 1 MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV 60

Query: 61 VPDCNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHWLVTDIKG 120
 VPDCNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHWLVTDIKG
 Sbjct: 61 VPDCNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHWLVTDIKG 120

Query: 121 ADLKKGKIQQQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRF 180
 ADLK+GKIQQQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRF
 Sbjct: 121 ADLKEGKIQQQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRF 180

Query: 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNAEIAAC 227
 LNRFLHGEPEASTQFMTQNYQDSPTLQAPR RASEPKHKNAEIAAC
 Sbjct: 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKNAEIAAC 227

>GSP:Y11860|Y11860|Human 5' EST secreted protein SEQ ID No: 460.
 Length = 121

Score = 258 bits (652), Expect = 6e-69
 Identities = 120/121 (99%), Positives = 120/121 (99%)

Query: 1 MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV 60
 MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV
 Sbjct: 1 MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV 60

Query: 61 VPDCNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHWLVTDIKG 120
 VPDC NYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHWLVTDIKG
 Sbjct: 61 VPDCXNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHWLVTDIKG 120

Query: 121 A 121
 A
 Sbjct: 121 A 121

>GSP:R27718|R27718|HCNP precursor protein #2.
 >GSP:R49943|R49943|Human hippocampal cholinergic
 neurotrophic peptide precursor. >PIR:I53745 I38109
 S52932 I56489
 S37554|I53745|phosphatidylethanolamine-binding protein -
 human >GNP:X75252|X75252_1|H.sapiens
 phosphatidylethanolamine binding protein mRNA.
 >GNP:X85033|X85033_1|H.sapiens mRNA for
 phosphatidylethanolamine binding protein.
 >GNP:D16111|D16111_1|Human mRNA for human homologue of
 rat phosphatidylethanolamine binding protein, complete
 cds.
 Length = 187

Score = 80.8 bits (196), Expect = 2e-15
 Identities = 43/124 (34%), Positives = 64/124 (50%), Gaps = 8/124 (6%)

Query: 79 VKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLKKGIQQQELSAYQA 138
 + + G G Y LV+ DPDAPSR +P+ R W H+LV ++KG D+ G + LS Y
 Sbjct: 53 ISWDGLDSGKLYTLVLTDPDAPSRKDPKYREWHHFLVVNMKGNDISSGTV----LSDYVG 108

Query: 139 PSPPAHSGFHRYQFFVYLQEGKVIS----LLPKENKTRGSWKMDRFLNRFLHGEPEASTQ 194
 PP +G HRY + VY Q+ + L + RG +K+ F ++ L P A T
 Sbjct: 109 SGPPKGTGLHRYVWLVEQDRPLKCDEPILSNRSGDHRGKFKVASFRKKYELRAPVAGTC 168

Query: 195 FMTQ 198
 + +
 Sbjct: 169 YQAE 172

>GSP:R64268|R64268|Phosphatidylethanolamine binding protein.

Length = 187

Score = 80.8 bits (196), Expect = 2e-15

Identities = 43/124 (34%), Positives = 64/124 (50%), Gaps = 8/124 (6%)

Query: 79 VKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLKKGKIQQQELSAYQA 138
 + + G G Y LV+ DPDAPSR +P+ R W H+LV ++KG D+ G + LS Y
 Sbjct: 53 ISWDGLDSGKLYTLVLTDPDAPSRKDPKYREWHHFLVVMKGNDISSGTV----LSDYVG 108

Query: 139 PSPPAHSGFHRYQFFVYLQEGKVIS----LLPKENKTRGSWKMDRFLNRFHLGEPEASTQ 194
 PP +G HRY + VY Q+ + L + RG +K+ F ++ L P A T
 Sbjct: 109 SGPPKGTGLHRYVWLVEQDRPLKCDEPILSNRSGDHRGKFKVASFRKKYELRAPVAGTC 168

Query: 195 FMTQ 198

+ +

Sbjct: 169 YQAE 172

>SP:P30086|PEBP_HUMAN|PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN
 (PEBP) (NEUROPOLYPEPTIDE H3).
 Length = 186

Score = 80.8 bits (196), Expect = 2e-15

Identities = 43/124 (34%), Positives = 64/124 (50%), Gaps = 8/124 (6%)

Query: 79 VKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLKKGKIQQQELSAYQA 138
 + + G G Y LV+ DPDAPSR +P+ R W H+LV ++KG D+ G + LS Y
 Sbjct: 52 ISWDGLDSGKLYTLVLTDPDAPSRKDPKYREWHHFLVVMKGNDISSGTV----LSDYVG 107

Query: 139 PSPPAHSGFHRYQFFVYLQEGKVIS----LLPKENKTRGSWKMDRFLNRFHLGEPEASTQ 194
 PP +G HRY + VY Q+ + L + RG +K+ F ++ L P A T
 Sbjct: 108 SGPPKGTGLHRYVWLVEQDRPLKCDEPILSNRSGDHRGKFKVASFRKKYELRAPVAGTC 167

Query: 195 FMTQ 198

+ +

Sbjct: 168 YQAE 171

>GNP:S76773|S76773_1|neuropolypeptide h3 [human, brain, mRNA
 Partial, 723 nt].
 Length = 140

Score = 80.8 bits (196), Expect = 2e-15

Identities = 43/124 (34%), Positives = 64/124 (50%), Gaps = 8/124 (6%)

Query: 79 VKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLKKGKIQQQELSAYQA 138
 + + G G Y LV+ DPDAPSR +P+ R W H+LV ++KG D+ G + LS Y
 Sbjct: 6 ISWDGLDSGKLYTLVLTDPDAPSRKDPKYREWHHFLVVMKGNDISSGTV----LSDYVG 61

Query: 139 PSPPAHSGFHRYQFFVYLQEGKVIS----LLPKENKTRGSWKMDRFLNRFHLGEPEASTQ 194
 PP +G HRY + VY Q+ + L + RG +K+ F ++ L P A T
 Sbjct: 62 SGPPKGTGLHRYVWLVEQDRPLKCDEPILSNRSGDHRGKFKVASFRKKYELRAPVAGTC 121

Query: 195 FMTQ 198

+ +

Sbjct: 122 YQAE 125

>GSP:Y11503|Y11503|Human 5' EST secreted protein SEQ ID No 325.
 Length = 120

Score = 35.2 bits (79), Expect = 0.090

Identities = 22/75 (29%), Positives = 37/75 (49%), Gaps = 6/75 (8%)

Query: 84 AVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLKKGKIQQQELSAYQAPSPPA 143
 A +G+ + L++ D EP + HWL+T+I G + +G++ Y P P
 Sbjct: 24 AEEGSLWTLTLLTSLDG-HLLEPDAEYL-HWLLTNIPGNRVAEGQVT----CPYLPPFFAR 77

Query: 144 HSGFHRYQFFVYLQE 158

SG HR F ++ Q+

Sbjct: 78 GSGIHLAFLFLFKQD 92

>STR:AAF28940|AAF28940|HSPC262 (Fragment).

>GNP:AF161380|AF161380_1|Homo sapiens HSPC262 mRNA,
 partial cds.
 Length = 174

Score = 35.2 bits (79), Expect = 0.090
 Identities = 22/75 (29%), Positives = 37/75 (49%), Gaps = 6/75 (8%)

Query: 84 AVDGATYILVMVDPDAPSRAPRQRFWRHWLVTDIKGADLKKGKIQQQELSAYQAPSPPA 143
 A +G+ + L++ D EP + HWL+T+I G + +G++ Y P P
 Sbjct: 2 AEEGSLWTLTLLTSLDG-HLLEPDAYL-HWLLTNIPGNRVAEGQVT----CPYLPPFPAR 55

Query: 144 HSGFHRYQFFVYLQE 158
 SG HR F ++ Q+
 Sbjct: 56 GSGIHLAFLFLFKQD 70

>STR:Q92508|Q92508|MYELOBLAST KIAA0233. >GNP:D87071|D87071_1|Human
 mRNA for KIAA0233 gene, complete cds; similar to
 C.elegans protein encoded in cosmid T20D3 (Z68220)..
 Length = 2035

Score = 30.1 bits (66), Expect = 3.0
 Identities = 22/64 (34%), Positives = 33/64 (51%), Gaps = 6/64 (9%)

Query: 97 PDAPSRAPR-QRFRHWL--VTDIKGAD--LKKGKIQQQELSAYQAPSPPAHSGFH-RY 150
 PD+P + P R+++WR WL T I D L + + +E + + P P A S F Y
 Sbjct: 903 PDSPPGSSPPRRQWRPWLHDATVIHSGDYFLFESDSEEEEEAVPEDPRPSAQSAFQLAY 962

Query: 151 QFFV 154
 Q +V
 Sbjct: 963 QAWV 966

Database: /nfs/banks2/index/data/blast/smartSorted/PROT/homosapiens
 Posted date: Oct 5, 2000 10:09 AM
 Number of letters in database: 24,820,038
 Number of sequences in database: 113,759

Lambda	K	H
0.319	0.136	0.425

Gapped		
Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 12826195
 Number of Sequences: 113759
 Number of extensions: 560821
 Number of successful extensions: 1270
 Number of sequences better than 10.0: 10
 Number of HSP's better than 10.0 without gapping: 7
 Number of HSP's successfully gapped in prelim test: 3
 Number of HSP's that attempted gapping in prelim test: 1259
 Number of HSP's gapped (non-prelim): 10
 length of query: 227
 length of database: 24,820,038
 effective HSP length: 47
 effective length of query: 180
 effective length of database: 19473365
 effective search space: 3505205700
 effective search space used: 3505205700
 T: 11
 A: 40
 X1: 16 (7.4 bits)
 X2: 38 (14.8 bits)
 X3: 64 (24.9 bits)
 S1: 41 (21.8 bits)
 S2: 62 (28.6 bits)